

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:48:45 ; Search time 7.04242 Seconds

(without alignments)  
1133.013 Million cell updates/sec

Title: US-09-988-971-2\_COPY\_94\_176

Perfect score: 446

Sequence: 1 WLYEGISREKNAEELLPQN.....WLYISPLTFPSLQALVDHY 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	254	57.0	505	1	TVHDC
2	242	54.3	512	1	TVHDC
3	241	54.0	503	1	JQ1321
4	241	54.0	512	1	I56160
5	241	54.0	512	1	A39719
6	240	53.8	281	2	A57152
7	240	53.8	503	1	TVHDC
8	232.5	52.1	505	2	I37206
9	228	51.1	509	1	OKHULK
10	227	50.9	509	1	I48845
11	224.5	50.3	499	1	A40092
12	223	50.0	507	1	A39939
13	217	48.7	544	2	I51593
14	215	48.2	537	1	A45501
15	214	48.0	528	1	TVFVG9
16	214	48.0	541	1	TVCHS
17	212	47.5	529	1	TVHUF8
18	212	47.5	543	1	TVHUF8
19	211	47.3	541	2	S31645
20	209	46.9	534	1	A44991
21	208	46.6	517	2	A43807
22	207	46.4	539	2	B49114
23	207	46.4	539	1	TVHUF8
24	206	46.2	534	1	S33568
25	206	46.2	537	1	TVHUF8
26	205	46.0	517	2	S24547
27	203	45.5	537	1	A43806
28	199	44.6	532	2	S04205
29	197	44.2	537	2	I51592

## ALIGNMENTS

30	197	44.2	542	2	A49114	protein-tyrosine k
31	195	43.7	536	2	S33569	protein-tyrosine k
32	186	41.7	526	1	TVFV60	protein-tyrosine k
33	186	41.7	533	1	TVCHS	protein-tyrosine k
34	186	41.7	557	1	TVFVS2	protein-tyrosine k
35	186	41.7	587	1	TVFVPR	protein-tyrosine k
36	185	41.5	568	1	TVFVS1	protein-tyrosine k
37	184.5	41.4	506	1	S24553	protein-tyrosine k
38	181	40.6	526	2	S26420	protein-tyrosine k
39	179	40.1	523	1	TVFVMT	protein-tyrosine k
40	179	40.1	545	2	S52313	protein-tyrosine k
41	179	40.1	546	2	S52314	protein-tyrosine k
42	177	39.7	526	1	TVFVPR	protein-tyrosine k
43	177	39.7	526	1	S15582	protein-tyrosine k
44	177	39.7	541	2	A43610	protein-tyrosine k
45	177	39.7	542	1	TVHUC	protein-tyrosine k

## RESULT 1

TVHUC  
protein-tyrosine kinase (EC 2.7.1.112) hck - human

C.Species: Homo sapiens (man)  
C.Date: 31-Dec-1989 #sequence\_revision 10-Nov-1995 #text\_change 11-Jun-1999

C.Accession: A27811; A27812; J01149; C38268; S31103

R.Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettinati, M.J.; Le Beau, M.M.; Diak

Mol. Cell. Biol. 7, 2267-2275, 1987

A.Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and

A.Reference number: A27811; PMID:87257942; PMID:3496523

A.Accession: A27811

A.Molecule type: mRNA

A.Residues: 1-505 <Q1>

A.Cross-references: GB:M16591

A.Note: the codon given for 3-Cys (TGC) is inconsistent with the authors' translation

Rizigler, S.F.; Marsh, J.D.; Lewis, D.B.; Perlmutter, R.M.

Mol. Cell. Biol. 7, 2276-2285, 1987

A.Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of b

A.Reference number: A27812; PMID:87257943; PMID:3453117

A.Accession: A27812

A.Molecule type: mRNA

A.Residues: 1-505 <Z1B>

A.Cross-references: GB:M16592; NID:9183913; PIDN:AA52644.1; PID:9306833

A.Hirshetzky, D.; Streibhardt, K.; Ruebsamen-Waigmann, H.

Gene 113, 275-280, 1992

A.Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase

A.Reference number: J01149; PMID:92241680; PMID:1572549

A.Accession: J01149

A.Molecule type: DNA

A.Residues: 157-505 <HRA>

A.Cross-references: EMBL:X59741

R.Partenen, J.; Maekela, T.P.; Allitalo, R.; Lehtvaestaho, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A.Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A.Reference number: A38268; PMID:91062389; PMID:2247464

A.Accession: C38268

A.Status: nucleic acid sequence not shown; not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 362-417 <PAR>

C.Genetics:

A.Gene: GDB:HCK

A.Cross-references: GDB:119303; OMIM:142370

A.Map position: 20q11-20q12

A.Functions: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1

C.Function:

A.Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho

P-2-505/Products: protein-tyrosine kinase hck #status predicted <Mat>

F:64-112/Domain: SH3 homology <SH3>

F:123-220/Domain: SH2 homology <SH2>

F:239-497/Domain: protein kinase homology <KIN>

RESULT 4  
I56160  
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

N.Contains: protein-tyrosine kinase lym, splice form B  
 C.Species: Rattus norvegicus (Norway rat)  
 C.Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
 C.Accession: 156160; 167811, 167812  
 R.Mingochi, K.; Nishikata, H.; Siraganian, R.P.  
 J. Immunol. 150, 222, 1993  
 A.Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leukaemia cells  
 A.Reference number: 156160  
 A.Accession: 156160  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-512 <MIN>  
 A.Cross-references: GB:LI4951; NID:9294582; PIDN:AAA41549.1; PID:9294583  
 R.Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.  
 Gene 138, 219-222, 1994  
 A.Title: The cDNAs encoding two forms of the lyn protein tyrosine kinase are expressed in rat basophilic leukemia cells  
 A.Reference number: 153715; MUID:9411041; PMID:8125304  
 A.Accession: 167811  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-230, 'V', 232-307, 'A', 309-418, 'Y', 420-512 <RID1>  
 A.Cross-references: GB:LI4782; NID:9294578; PIDN:AAA20944.1; PID:9294579  
 A.Note: in Genbank entry RALVNAVTR, release 116.0, PIDN:AAA20944.1, the source is designating the protein-tyrosine kinase lym, splice form B #status predicted <MAT>  
 A.Accession: 167812  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-24, 46-230, 'V', 232-307, 'A', 309-418, 'Y', 420-512 <RID2>  
 A.Cross-references: GB:LI4823; NID:9294580; PIDN:AAA20945.1; PID:9294581  
 A.Note: in Genbank entry RALVNAVTR, release 116.0, PIDN:AAA20945.1, the source is designating the protein-tyrosine kinase src; protein kinase homology; SH3 homology; SH3 h C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein F.12-512/Product: protein-tyrosine kinase lym, splice form A #status predicted <MAT>  
 F.2-24, 46-512/Product: protein-tyrosine kinase lym, splice form B #status predicted <MAT>  
 F.70-118/Domain: SH3 homology <SH3>  
 F.129-226/Domain: SH2 homology <SH2>  
 F.245-504/Domain: protein kinase homology <KIN>  
 F.253-261/Region: protein kinase ATP-binding motif  
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F.275/Active site: Lys #status predicted  
 F.397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 54.0%; Score 241; DB 1; Length 512;  
 Best Local Similarity 54.2%; Pred. No. 1.1e-19;  
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 60  
 DB 129 WPFKDIRKDAERQLAPGNSAGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 188  
 QY 61 DNGMLYSPRLTFPSLQALVDHY 83  
 DB 189 DNGGYISPRITFPCLSDIMIKHY 211

RESULT 5  
 A39719  
 protein-tyrosine kinase (EC 2.7.1.112) lym, long splice form - mouse  
 N.Contains: protein-tyrosine kinase lym, short splice form  
 C.Species: Mus musculus (house mouse)  
 C.Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 03-Mar-2000  
 C.Accession: A39719; B39719; A39750; B39750  
 R.Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.  
 Mol. Cell. Biol. 11, 3399-3406, 1991  
 A.Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.  
 A.Reference number: A39719; MUID:91260688; PMID:11710766  
 A.Accession: A39719  
 A.Molecule type: mRNA  
 A.Residues: 1-512 <STA1>  
 A.Cross-references: GB:M64608; NID:9198938; PIDN:AAA39470.1; PID:9198939  
 A.Accession: B39719  
 A.Molecule type: mRNA  
 A.Residues: 1-24, 46-512 <STA2>  
 A.Cross-references: GB:M64608

R.Yi, T.; Bolen, J.B.; Ihle, J.N.  
 Mol. Cell. Biol. 11, 2391-2398, 1991  
 A.Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids  
 A.Reference number: A39750; MUID:91203857; PMID:2017160  
 A.Accession: A39750  
 A.Molecule type: mRNA  
 A.Residues: 1-76, 'P', 78-160, 'I', 162-278, 'V', 280-390, 'I', 392-424, 'D', 426-512 <Y11>  
 A.Cross-references: GB:M57697; NID:9198942; PIDN:AAA39472.1; PID:9198943  
 A.Coverage: 100%  
 C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein F.1-512/Product: protein-tyrosine kinase lym, long splice form #status predicted <MAT>  
 F.1-24, 46-512/Product: protein-tyrosine kinase lym, short splice form #status predicted <MAT>  
 F.70-118/Domain: SH3 homology <SH3>  
 F.129-226/Domain: SH2 homology <SH2>  
 F.245-504/Domain: protein kinase homology <KIN>  
 F.253-261/Region: protein kinase ATP-binding motif  
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F.275/Active site: Lys #status predicted  
 F.397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 54.0%; Score 241; DB 1; Length 512;  
 Best Local Similarity 54.2%; Pred. No. 1.1e-19;  
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 60  
 DB 129 WPFKDIRKDAERQLAPGNSAGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 188  
 QY 61 DNGMLYSPRLTFPSLQALVDHY 83  
 DB 189 DNGGYISPRITFPCLSDIMIKHY 211

RESULT 6  
 A57152  
 src-like adaptor protein - mouse  
 C.Species: Mus musculus (house mouse)  
 C.Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 12-Feb-1999  
 C.Accession: A57152  
 J.Pandey, A.; Duan, H.; Dixit, V.M.  
 J. Biol. Chem. 270, 19201-19204, 1995  
 A.Title: Characterization of a novel Src-like adapter protein that associates with the E6 oncoprotein  
 A.Reference number: A57152; MUID:95370243; PMID:7543898  
 A.Accession: A57152  
 A.Status: preliminary; not compared with conceptual translation  
 A.Molecule type: mRNA  
 A.Residues: 1-281 <PAN>  
 A.Cross-references: GB:U29056  
 C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein F.12-512/Product: protein-tyrosine kinase lym, long splice form #status predicted <MAT>  
 F.1-24, 46-512/Product: protein-tyrosine kinase lym, short splice form #status predicted <MAT>  
 F.70-118/Domain: SH3 homology <SH3>  
 F.129-226/Domain: SH2 homology <SH2>

Query Match 53.8%; Score 240; DB 2; Length 281;  
 Best Local Similarity 57.8%; Pred. No. 7.1e-20;  
 Matches 48; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

QY 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 60  
 DB 84 WLVEGSRKAEELLPGNPGAFILRESQTRGSYSLSVLRSPASMDRIHYRHCL 137  
 QY 61 DNGMLYSPRLTFPSLQALVDHY 83  
 DB 138 PNMWYISPRITFPCLSDIMIKHY 160

RESULT 7  
 TMSHC  
 protein-tyrosine kinase (EC 2.7.1.112) hck - mouse  
 N.Alternate names: kinase-related transforming protein (bmk)

C/Species: Mus musculus (house mouse)  
 C/Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 28-Jan-2000  
 C/Accession: A27282; A39973  
 R/Klemenz, M.J.; McKercher, S.R.; Maki, R.A.  
 Nucleic Acids Res. 15, 9600, 1987  
 A/Title: Nucleotide sequence of the mouse hck gene.  
 A/Reference number: A27282; MUID:86067781; PMID:3684607  
 A/Accession: A27282  
 A/Molecule type: mRNA  
 A/Residues: 1-503 <KLE>  
 A/Cross-references: GB:Y00487; NID:951209; PIDN:CA68544.1; PID:951210  
 R/Holzman, D.A.; Cook, W.D.; Dunn, A.R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987  
 A/Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed  
 A/Reference number: A39973; MUID:86065587; PMID:3317404  
 A/Accession: A39973  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-503 <HOL>  
 A/Cross-references: GB:J03023; NID:9192212; PIDN:AAA37305.1; PID:9309118.  
 C/Genetics:  
 A/Gene: hck  
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h  
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho  
 F:62-110/Domain: SH3 homology <SH3>  
 F:121-218/Domain: SH2 homology <SH2>  
 F:237-495/Domain: protein kinase homology <KIN>  
 F:245-253/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F:267/Active site: Lys #status predicted  
 F:388-499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 53.8%; Score 240; DB 1; Length 503;  
 Best Local Similarity 56.6%; Pred. No. 1.4e-19;  
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

Qy 1 WLVEGSRKAEELLRLPGNPGAFIRSGSYSLVSLSPASNDRIHYRHCL 60  
 Db 121 WFKGISRKAEKRLHLPNGMGSFPIRDSFTTGSLSVSDPDQGHDTVKKYKIRTL 180

Qy 61 DNGWLYSPRLTFPSLQALVDHY 83  
 Db 181 DSGGYISPRITFPSLQALVDHY 203

RESULT 8  
 137206  
 protein-tyrosine kinase (EC 2.7.1.112) b1k - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 04-Mar-2000  
 C/Accession: I37206; S51647  
 R/Irlam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.  
 J. Immunol. 154, 1265-1272, 1995  
 A/Title: Molecular cloning, characterization, and chromosomal localization of a human ty  
 A/Reference number: I37206; MUID:95123078; PMID:7822795  
 A/Accession: I37206  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-505 <RES>  
 A/Cross-references: EMBL:Z33998; NID:9601951; PIDN:CA63965.1; PID:9601952  
 C/Genetics:  
 A/Gene: GDB:B1K  
 A/Cross-references: GDB:454114; OMIM:191305  
 A/Map position: 8p23-8p22  
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h  
 C/Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro  
 F:65-113/Domain: SH3 homology <SH3>  
 F:124-220/Domain: SH2 homology <SH2>  
 F:239-497/Domain: protein kinase homology <KIN>  
 F:247-255/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:269/Active site: Lys #status predicted

Query Match 52.1%; Score 232.5; DB 2; Length 505;  
 Best Local Similarity 54.2%; Pred. No. 1e-18;  
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

Qy 1 WLVEGSRKAEELLRLPGNPGAFIRSGSYSLVSLSPASNDRIHYRHCL 60  
 Db 124 WFKGISRKAEKRLHLPNGMGSFPIRDSFTTGSLSVSDPDQGHDTVKKYKIRTL 182

Qy 61 DNGWLYSPRLTFPSLQALVDHY 83  
 Db 183 DSGGYISPRITFPSLQALVDHY 205

RESULT 9  
 OKRULK  
 protein-tyrosine kinase (EC 2.7.1.112) lck - human  
 N/Alternate names: kinase-related transforming protein (lck)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 28-Jan-2000  
 C/Accession: J00152; S07822; S07200; S01879; S01143; A32797; I57636  
 R/Bouet, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.  
 Gene 84, 105-113, 1989  
 A/Title: Structure of the human lck gene: differences in genomic organization within src  
 A/Reference number: J00152; MUID:90108697; PMID:2558056  
 A/Accession: J00152  
 A/Molecule type: DNA  
 A/Residues: 1-509 <ROU>  
 A/Cross-references: EMBL:X14053  
 R/Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.  
 J. Cell. Biochem. 39, 117-126, 1988  
 A/Title: Structure and expression of lck transcripts in human lymphoid cells.  
 A/Reference number: S07822; MUID:89123626; PMID:3265417  
 A/Accession: S07822  
 A/Molecule type: mRNA  
 A/Residues: 1-86; 'P', 88-509 <PER>  
 A/Cross-references: EMBL:X13529; NID:934294; PIDN:CA61884.1; PID:934295  
 R/Koga, Y.; Gacalia, N.; Toyonaga, B.; Spolek, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.  
 Eur. J. Immunol. 16, 1643-1646, 1986  
 A/Title: A human T cell-specific cDNA clone (Y116) encodes a protein with extensive hom  
 A/Reference number: S07200; MUID:87133811; PMID:343153  
 A/Accession: S07200  
 A/Molecule type: mRNA  
 A/Residues: 1-205; 'ASATPT', 212-257, 'RCGM', 262, 'TTT', 266, 'T', 268-281, 'AGRLP', 287-503, 'ST  
 A/Cross-references: EMBL:X05027; NID:936807; PIDN:CA28691.1; PID:936808  
 R/Veilleux, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.  
 Oncogene Res. 1, 357-374, 1987  
 A/Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n  
 A/Reference number: S01879; MUID:88217332; PMID:2855736  
 A/Accession: S01879  
 A/Molecule type: mRNA  
 A/Residues: 368-471, 'H', 473-509 <VEI>  
 A/Cross-references: EMBL:X06369; NID:934288; PIDN:CA29667.1; PID:934289  
 R/Trevelyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canina, C.; Linna, T.J.  
 Biochim. Biophys. Acta 888, 286-295, 1986  
 A/Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA)  
 A/Reference number: S07143; MUID:87000726; PMID:3469486  
 A/Accession: S07143  
 A/Molecule type: mRNA  
 A/Residues: 'A', 376-509 <TRE>  
 A/Cross-references: EMBL:X04476; NID:935779; PIDN:CA28165.1; PID:935780  
 R/Takdera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.  
 Mol. Cell. Biol. 9, 2173-2180, 1989  
 A/Title: Structure of the two promoters of the human lck gene: differential accumulation  
 A/Reference number: A32797; MUID:89313764; PMID:2787474  
 A/Accession: A32797  
 A/Molecule type: DNA  
 A/Residues: 1-35 <TK>  
 A/Cross-references: GB:M26692; NID:9341523; PIDN:AAA59503.1; PID:9349702  
 R/Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.  
 Mol. Cell. Biol. 8, 3058-3064, 1988  
 A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel  
 A/Reference number: I57636; MUID:89036891; PMID:2850479

A:Accession: 157636  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-35, 'VR' <RES>  
 A:Cross-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522  
 C:Comment: Protein tyrosine kinases play important roles in the control of cell growth and cell division  
 C:Genetics:  
 A:Gene: GDB:LCK  
 A:Cross-references: GDB:119360; OMIM:153390  
 A:Map position: 1p35-1p34.3  
 A:Introns: 35/3, 63/1, 93/2, 126/2, 161/1, 211/1, 262/1, 322/1, 347/3, 399/1, 443/1  
 C:Function:  
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc  
 F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>  
 F:68-116/Domain: SH3 homology <SH3>  
 F:127-224/Domain: SH2 homology <SH2>  
 F:243-501/Domain: protein kinase homology <KIN>  
 F:251-259/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:3/5/Binding site: palmitate (Cys) (covalent) #status predicted  
 F:273/Active site: Lys #status predicted  
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 51.1%; Score 228; DB 1; Length 509;  
 Best Local Similarity 54.2%; Pred. No. 3.3e-18;  
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Qy 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSGVSLVRSPASMDIRHYRHICL 60  
 Db 127 WFFKNLSRKDAERQLAPGNTHGSLFIRESESTAGSFSLSRDPDQNGEVVYKXIKRL 166

Qy 61 DNGMLYISPRITFPLQALVDHY 83  
 Db 187 DNGFYISPRITFPLGLDLVYHY 209

RESULT 10  
 148845  
 protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse  
 N:Alternate names: p56, protein-tyrosine kinase cck  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 03-Mar-2000  
 A:Accession: 148845; A23639; 157629; 177452  
 R:Voronoval, A.F.; Sefton, B.M.  
 Nature 319, 682-685, 1986  
 A>Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote  
 A:Reference number: 148845; MUID:86146842; PMID:3081813  
 A:Accession: 148845  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-509 <VOR1>  
 A:Cross-references: EMBL:X03533; NID:g54813; PIDN:CAA27234.1; PID:g54814  
 R:March, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.  
 Cell 43, 393-404, 1985  
 A>Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed  
 A:Reference number: A23639; MUID:86079521; PMID:2416464  
 A:Accession: A23639  
 A:Molecule type: mRNA  
 A:Residues: 1-282, 'VP', 285-509 <MAR>  
 A:Cross-references: GB:M2056; NID:g198763  
 A>Note: The sequence is revised in Genbank entry M2056, release 116.0, (PIDN:AA59674.1  
 R:Voronoval, A.F.; Adler, H.T.; Sefton, B.M.  
 Mol. Cell. Biol. 7, 4407-4413, 1987  
 A>Title: Two lck transcripts containing different 5' untranslated regions are present in  
 A:Reference number: 157629; MUID:88142832; PMID:3501824  
 A:Accession: 157629  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-11 <VOR>  
 A:Cross-references: GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:g198767  
 R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.

Mol. Cell. Biol. 8, 3058-3064, 1988  
 A>Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell  
 A:Reference number: 157636; MUID:89096891; PMID:2850479  
 A:Accession: 177452  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-35, 'VR' <GAR>  
 A:Cross-references: GB:M21511; NID:g198766; PIDN:AAA39422.1; PID:g554186  
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
 C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming protein  
 F:68-116/Domain: SH3 homology <SH3>  
 F:127-224/Domain: SH2 homology <SH2>  
 F:243-501/Domain: protein kinase homology <KIN>  
 F:251-259/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:273/Active site: Lys #status predicted  
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 50.9%; Score 227; DB 1; Length 509;  
 Best Local Similarity 54.2%; Pred. No. 4.3e-18;  
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Qy 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSGVSLVRSPASMDIRHYRHICL 60  
 Db 127 WFFKNLSRKDAERQLAPGNTHGSLFIRESESTAGSFSLSRDPDQNGEVVYKXIKRL 166

Qy 61 DNGMLYISPRITFPLQALVDHY 83  
 Db 187 DNGFYISPRITFPLGLDLVYHY 209

RESULT 11  
 A40092  
 protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 16-Jun-2000  
 A:Accession: A40092  
 R:Dymacki, S.M.; Niederhuber, J.E.; Desiderio, S.V.  
 Science 247, 332-336, 1990  
 A>Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.  
 A:Reference number: A40092; MUID:90117147; PMID:2404338  
 A:Accession: A40092  
 A:Molecule type: mRNA  
 A:Residues: 1-499 <DVA>  
 A:Cross-references: GB:M30903; NID:g202076; PIDN:AAA40453.1; PID:g202077  
 C:Genetics:  
 A:Gene: MGI:BLK  
 A:Cross-references: MGI:88169  
 A:Map position: 14:28.0  
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc  
 F:59-107/Domain: SH3 homology <SH3>  
 F:118-214/Domain: SH2 homology <SH2>  
 F:233-491/Domain: protein kinase homology <KIN>  
 F:241-249/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:263/Active site: Lys #status predicted

Query Match 50.3%; Score 224.5; DB 1; Length 499;  
 Best Local Similarity 51.8%; Pred. No. 8.1e-18;  
 Matches 43; Conservative 16; Mismatches 23; Indels 1; Gaps 1;

Qy 1 WLVEGSRKAEELLPGNPGAFILRESQTRGSGVSLVRSPASMDIRHYRHICL 60  
 Db 118 WFFRTISRKDAERQLAPGNTHGSLFIRESESTAGSFSLSRDPDQNGEVVYKXIKRL 176

Qy 61 DNGMLYISPRITFPLQALVDHY 83  
 Db 177 DNGFYISPRITFPLGLDLVYHY 199

RESULT 12  
 A39939

protein-tyrosine kinase (EC 2.7.1.112) tk1 [similarity] - chicken  
 N/Alternate names: Kinase-related transforming protein (tk1); T-cell surface antigen a55  
 C/Species: Gallus gallus (chicken)  
 C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 16-Jun-2000  
 C/Accession: A42126; A39939  
 R/Crow, L.M.; Ratcliffe, M.J.; Veilleux, A.  
 M/1. Cell. Biol. 12, 1226-1233, 1992  
 A/Title: tk1 is the avian homolog of the mammalian lck tyrosine protein kinase gene.  
 A/Reference number: A42126; PMID:92186854; PMID:1545804  
 A/Accession: A42126  
 A/Molecule type: mRNA  
 A/Residues: 1-88 <CHO>  
 A/Cross-references: GB:W85043  
 A/Experimental source: thymus, spleen  
 A/Note: sequence extracted from NCBI Backbone (NCBI:88831, NCBI:88833)  
 R/Strebhardt, K.; Mullins, J.D.; Bruck, C.; Rubeamen-Waligmann, H.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987  
 A/Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related  
 A/Reference number: A39939; PMID:88097370; PMID:3321053  
 A/Accession: A39939  
 A/Molecule type: mRNA  
 A/Residues: 52-507 <STR>  
 A/Cross-references: GB:003579; NID:9212712; PIDN:AAA49081.1; PID:9212713  
 C/Suprafamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h  
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc  
 F:66-114/Domain: SH3 homology <SH3>  
 F:125-222/Domain: SH2 homology <SH2>  
 F:241-499/Domain: protein kinase homology <KIN>  
 F:249-257/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 50.0%; Score 223; DB 1; Length 507;  
 Best Local Similarity 53.0%; Pred. No. 1.2e-17;  
 Matches 44; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Oy 1 WYEGSLREKAEELLLPONGGAFILRESQTRGYSLSVLRSPASMDRIRHRIHCL 60  
 Db 125 WPKULSRKNEARLLPNSGTHSFLRESSTSGYSLSVDFPONGGTVVHKKIRRM 184  
 Oy 61 DNGWLYSPRLTSPSLQALVDHY 83  
 Db 185 DNGGYISPRVTFSSLHEVEY 207

RESULT 13  
 I51593  
 Protein-tyrosine kinase (EC 2.7.1.112) yes - Xiphophorus helleri  
 C/Species: Xiphophorus helleri  
 C/Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 18-Feb-2000  
 C/Accession: I51593  
 R/Hannig, G.; Ottliffe, S.; Schartl, M.  
 Oncogene 6, 361-369, 1991  
 A/Title: Conservation of structure and expression of the c-yes and fyn genes in lower ve  
 A/Reference number: I51592; PMID:91187435; PMID:1707152  
 A/Accession: I51593  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-544 <HAN>  
 A/Cross-references: EMBL:X54970; NID:G64483; PIDN:CAA38714.1; PID:G64484  
 C/Genetics:  
 A/Gene: Yyes  
 C/Suprafamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h  
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc  
 F:99-148/Domain: SH3 homology <SH3>  
 F:159-256/Domain: SH2 homology <SH2>  
 F:276-534/Domain: protein kinase homology <KIN>  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:306/Active site: lys #status predicted  
 F:427,538/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 48.7%; Score 217; DB 2; Length 544;  
 Best Local Similarity 54.2%; Pred. No. 6.5e-17;

Matches 45; Conservative 9; Mismatches 29; Indels 0; Gaps 0;

Oy 1 WYEGSLREKAEELLLPONGGAFILRESQTRGYSLSVLRSPASMDRIRHRIHCL 60  
 Db 159 WPKULSRKNEARLLPNSGTHSFLRESSTSGYSLSVDFPONGGTVVHKKIRRM 218  
 Oy 61 DNGWLYSPRLTSPSLQALVDHY 83  
 Db 219 DNGGYISPRVTFSSLHEVEY 241

RESULT 14  
 A45501  
 protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog  
 N/Alternate names: Kinase-related transforming protein (yes)  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 16-Jun-2000  
 C/Accession: A45501; S08517  
 R/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.  
 Oncogene Res. 1, 223-233, 1989  
 A/Title: The yes proto-oncogene is present in amphibians and contributes to the maternal  
 A/Reference number: A45501  
 A/Accession: A45501  
 A/Molecule type: mRNA  
 A/Residues: 1-537 <STR>  
 A/Cross-references: GB:X14377  
 R/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.  
 submitted to the EMBL Data Library, February 1989  
 A/Reference number: S08517  
 A/Accession: S08517  
 A/Molecule type: mRNA  
 A/Residues: 1-250; S:252-537 <STR>  
 A/Cross-references: EMBL:X14377; NID:G65272; PIDN:CAA32551.1; PID:G65273  
 C/Genetics:  
 A/Gene: yes  
 C/Suprafamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h  
 C/Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro  
 F:92-141/Domain: SH3 homology <SH3>  
 F:152-249/Domain: SH2 homology <SH2>  
 F:269-527/Domain: protein kinase homology <KIN>  
 F:277-285/Region: protein kinase ATP-binding motif  
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F:299/Active site: lys #status predicted  
 F:420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 48.2%; Score 215; DB 1; Length 537;  
 Best Local Similarity 50.0%; Pred. No. 1.1e-16;  
 Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

Oy 1 WYEGSLREKAEELLLPONGGAFILRESQTRGYSLSVLRSPASMDRIR-----HY 55  
 Db 152 WYEGGKGRKAEELLLPNSGTHSFLRESSTSGYSLSVDFPONGGTVVHKKIRRM 206  
 Oy 56 RHCLDNGWLYSPRLTSPSLQALVDHY 83  
 Db 207 KIRKLDNGGYITTTAAGFESLQKLVKHY 234

RESULT 15  
 I79FVG9  
 protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73  
 C/Species: avian sarcoma virus Y73  
 A/Note: host Gallus gallus (chicken)  
 C/Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 23-Feb-1997  
 C/Accession: A00633  
 R/Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.  
 Nature 297, 205-208, 1982  
 A/Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its trans  
 A/Reference number: A00633; PMID:82195528; PMID:6281656  
 A/Accession: A00633  
 A/Molecule type: genomic RNA  
 A/Residues: 1-528 <KIT>  
 C/Comment: This protein is synthesized as a gag-yes polypeptide.

A;Gene:♦yes

**Cysuperfamily:** protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
**Keywords:** ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; transmembrane protein; tyrosine kinase; tyrosine phosphorylation  
**EC:** 2.7.1.17/kinase src homology src

F;148-245/Domain: SH2 homology <SH2>

F:273-281/Region: protein kinase ATP-binding motif

F.295/Active site: Lys #status predicted  
F.416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	48.0%;	Score 214;	DB 1;	Length 528;
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best local similarity 50.0%; Pred. NO. 1.4e-16;  
Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

QY 1 WLYEGLSREKAEELLLPNCGANFLIRESQTRRGSSYSLSVRLSRPASWDRIR-----HY 55

Db 148 WYFGKMGKDAERLLNPNQRCIFLVRESETTGAYSLIR----DWDEVGDNVKHY 2022

QY 56 RHCLDNGWLYISPRLTSPSLQALVDHY 83

Db 203 KIRKLDNGGYITTRAQFESLQKLVKHY 230

Search completed: March 24, 2003, 15:51:41  
Job time : 8.04242 secs

Job time : 8.04242 secs

